

CT Check Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Amino Acid Sequence

Arginine

Bacteriophages

Base Sequence

Circular Dichroism

Conserved Sequence

*Cytochrome b: BI, biosynthesis

*Cytochrome b: CH, chemistry

Databases, Factual

Enzyme-Linked Immunosorbent Assay

Genetic Vectors

Hemerythrin: AA, analogs & derivatives

Hemerythrin: BI, biosynthesis

Hemerythrin: CH, chemistry

Models, Structural

Molecular Sequence Data

Mutagenesis, Site-Directed

Oligodeoxyribonucleotides

Protein Folding

*Protein Structure, Secondary

Proteins: BI, biosynthesis

*Proteins: CH, chemistry

Random Allocation

Recombinant Proteins: BI, biosynthesis

Recombinant Proteins: CH, chemistry

Serine

Serum Albumin, Bovine

Tryptophan

RN 56-45-1 (Serine); 73-22-3 (Tryptophan); 74-79-3 (Arginine); 9035-37-4 (Cytochrome b); 9064-79-3 (cytochrome b562, E coli)

CN 0 (Genetic Vectors); 0 (Hemerythrin); 0 (Oligodeoxyribonucleotides); 0 (Proteins); 0 (Recombinant Proteins); 0 (Serum Albumin, Bovine); 0 (myohemerythrin)

=> d his

(FILE 'HOME' ENTERED AT 13:07:46 ON 09 JUL 2003)
SET COST OFF

FILE 'HCAPLUS' ENTERED AT 13:07:58 ON 09 JUL 2003

L1 1 S US20020048776/PN
L2 6 S (WO9726277 OR WO9116683 OR WO9321206 OR US5557535 OR WO930148
L3 1 S GOEDE ?/AU AND 1997/PY AND (18 AND 9 AND 1113)/SO

FILE 'WPIX' ENTERED AT 13:15:16 ON 09 JUL 2003

L4 6 S (WO9726277 OR US5495423 OR WO9116683 OR WO9321206 OR US555753

FILE 'MEDLINE' ENTERED AT 13:15:36 ON 09 JUL 2003

L5 1 S PREISSNER ?/AU AND 1998/PY AND (280 AND 3 AND 535)/SO

FILE 'WPIX' ENTERED AT 13:16:03 ON 09 JUL 2003

L6 1 S US20020048776/PN
E FROMMEL C/AU
L7 3 S E3
E PREISSNER R/AU
L8 3 S E3
E GOEDE A/AU
L9 4 S E3, E4
E JERINI/PA
L10 11 S E3-E7

L11 E FROEMMEL/AU
 7 S E5
 L12 1 S L4,L6 AND L7-L11
 L13 18 S L7-L11 NOT L12
 L14 7 S L4,L6,L12

FILE 'WPIX' ENTERED AT 13:26:40 ON 09 JUL 2003

FILE 'HCAPLUS' ENTERED AT 13:26:57 ON 09 JUL 2003

 E PREISSNER C/AU
 E PREISSNER R/AU
 L15 18 S E3,E4
 E FROMMEL C/AU
 L16 16 S E3,E5
 E FROEMMEL C/AU
 L17 43 S E3,E4
 E GOEDE A/AU
 L18 63 S E3-E6,E9,E10
 E JERINI/PA,CS
 L19 36 S E3-E22
 L20 2 S L1-L3 AND L15-L19
 L21 8 S L1-L3,L20
 L22 149 S L15-L19 NOT L21
 E LIGAND/CT
 E E38+ALL
 L23 15338 S E1
 L24 30095 S E1+NT
 L25 1 S L21 AND L23,L24
 L26 8 S L21,L25
 L27 0 S L22 AND L23,L24
 L28 5 S L22 AND LIGAND
 E PEISSNER R/AU
 L29 1' S E4 AND L28
 L30 5 S L28,L29
 SEL DN AN 4 5
 L31 2 S L30 AND E1-E6
 L32 10 S L26,L31
 L33 343188 S L23,L24 OR LIGAND
 L34 101010 S L33 AND (?PEPTIDE? OR ?PROTEIN? OR ENZYM? OR AMINO ACID?)
 L35 21636 S L33 AND (PEPTIDE? OR PROTEIN? OR ENZYM? OR AMINO ACID?)/SX,SC
 L36 48827 S L33 AND (PEPTIDE? OR PROTEIN? OR ENZYM? OR AMINO(L)ACID?)/CW
 L37 103800 S L34-L36
 E SECONDARY STRUCTURE/CT
 L38 6956 S E3,E4
 E E3+ALL
 L39 24837 S E4,E3+NT
 L40 1318 S L37 AND L38,L39
 L41 1021 S L37 AND SECONDARY STRUCTURE
 L42 1776 S L40,L41
 E E1+ALL
 L43 21752 S E2,E3,E1+NT AND L37
 L44 1601 S L42 AND L43
 L45 1776 S L42,L44
 E MOLECULAR SURFACE/CT
 E E3+ALL
 L46 367 S E3
 E E4+ALL
 L47 322 S E2+NT
 E E5+ALL
 L48 4867 S E2+NT
 E E15+ALL
 E MOLECULAR SURFACE/CT
 E E4+ALL

L49 706 S E2
L50 14 S L45 AND (L46-L49 OR MOLECULAR SURFACE)
SEL DN AN 3 6 10 11 14
L51 5 S L50 AND E1-E15
L52 32 S L45 AND (PROTEIN SURFACE OR SURFACE AREA)
L53 27 S L52 NOT L50
L54 1 S L53 AND PROTEIN SURFACE RECOGNITION
L55 6 S L51,L54
E MOLECULAR RECOGNITION/CT
E E3+ALL
L56 8689 S E2,E1+NT
E E6+ALL
L57 80573 S E1+NT
E E17+ALL
L58 4443 S E4,E3+NT
E E15+ALL
L59 549 S E2
L60 359 S L45 AND L56-L59
L61 15 S L60 AND (DRUG SCREENING+NT OR SCREENING+NT OR HIGH THROUGHPUT
L62 11 S L60 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES
L63 18 S L61,L62
L64 3 S L32 AND L33-L63
L65 14 S L32,L55,L64
L66 9 S L65 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES
L67 14 S L65,L66
L68 35 S L45 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES
E MODEL/CT
E E6+ALL
E E2+ALL
E E2+ALL
L69 179 S L45 AND E3-E5,E2+NT
L70 25 S L45 AND E39+NT
L71 16 S L45 AND E41+NT
E MODEL/CT
E E6+ALL
E E2+ALL
L72 208 S L68-L71
L73 22 S L72 AND LIGAND?/CW
L74 34 S L67,L73
L75 23 S L72 AND L74
L76 34 S L74,L75
L77 21 S L76 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)
L78 13 S L76 NOT L77
L79 87 S L72 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)
L80 76 S L79 NOT L77
SEL DN AN 2 23 41 74 75
L81 5 S L80 AND E1-E15
L82 26 S L77,L81
L83 26 S L82 AND L1-L3,L15-L82
L84 26 S L83 AND (SCREEN? OR SECOND? OR STRUCTUR? OR MOLECUL? OR SURFA
L85 23 S L84 AND (AMINO ACID OR CONFORM? OR FOLD?)
L86 26 S L84,L85

FILE 'HCAPLUS' ENTERED AT 14:16:12 ON 09 JUL 2003

FILE 'MEDLINE' ENTERED AT 14:16:42 ON 09 JUL 2003

E PROTEIN STRUCTURE/CT
E E12+ALL
L87 32663 S E10+NT
E DATABASE/CT
E E35+ALL
L88 815 S E6+NT AND L87
L89 410 S L88 AND PY<=1999

L90 19542 S L87 AND PY<=1999
L91 14192 S L1./CT AND L90
L92 14192 S L89,L91
E MOLECULAR SURFACE/CT
E E1+ALL
L93 13229 S E8+NT AND L92
E E80+ALL
L94 4712 S E4+NT AND L92
L95 1044 S LIGAND AND L92
L96 1018 S L95 AND L93,L94
E LIGANDS/CT
E E3+ALL
L97 476 S E7 AND L90
L98 1440 S LIGAND AND L90
L99 1440 S L97,L98,L95
L100 1359 S L99 AND D12./CT
L101 536 S L99 AND D8./CT
L102 1433 S L100,L101
E CONFORMATION/CT
E E8+ALL
L103 1433 S L102 AND E2+NT
E E2+ALL
L104 13 S L103 AND L88
SEL DN AN 1 5 7 8 9 11-13
L105 8 S L104 AND E1-E24
E BINDING SITES/CT
E E3+ALL
L106 172215 S E4+NT
E E26+ALL
L107 105279 S E7+NT
L108 5586 S L90 AND L106,L107
L109 809 S L108 AND L99
L110 7 S L109 AND L88
L111 594 S L109 AND L93,L94
L112 805 S L109 AND L103
L113 10 S L105,L110 AND L87-L112
E FROMMEL C/AU
L114 45 S E3,E4
E FROEMMEL C/AU
L115 3 S E3,E4
E PREISSNER R/AU
L116 14 S E3,E4
E GOEDE A/AU
L117 18 S E3-E8
L118 64 S L114-L117
L119 17 S L118 AND L87-L113
SEL DN AN 2-5 8 10-12
L120 8 S E1-E24
L121 17 S L113,L120 AND L87-L120
L122 56 S L118 NOT L121
SEL DN AN 14 22
L123 3 S E24-E30
L124 19 S L121,L123 AND L87-L123
L125 19 S L5,L124

FILE 'MEDLINE' ENTERED AT 14:34:11 ON 09 JUL 2003